21. (Amended) A method for identifying the presence of cancerous cells in a human sample wherein said method comprises:

(a) determining the quantity of hTERT mRNA in said sample and in a control sample of non cancerous cells by:

(1) contacting RNA from said sample and said control sample with a pair of primers, wherein said pair of primers consists of a first primer capable of hybridizing within exon 8 or downstream of exon 8 of the hTERT gene and a second primer capable of hybridizing upstream of exon 8 of the hTERT gene;

(2) amplifying the nucleic acid sequence;

(3) measuring the generation of amplification products;

(4) determining the quantity of hTERT mRNA in said sample from the results obtained in step (3); and

(b) identifying the presence of cancerous cells in said sample if the quantity of hTERT mRNA in said sample is greater than the quantity of hTERT mRNA in said control sample.

Please add the following new claims:

28. (New) The method of Claim 21, wherein said second primer is capable of hybridizing within exon 6 of the hTERT gene.

29. (New) The method of Claim 21, wherein said second primer is capable of hybridizing within exon 7 of the hTERT gene.

30. (New) The method of Claim 21, wherein said second primer is SYC1118 (SEQ ID NO:5) or SYC1076 (SEQ ID NO:2).

31. (New) The method of Claim 21, wherein the first primer is capable of hybridizing within exon 8.

32. (New) The method of Claim 31, wherein said first primer is SYC1097 (SEQ ID NO:4).

33. (New) The method of Claim 21, wherein the first primer is capable of hybridizing within exon 9.

34. (New) The method of Claim 33, wherein the first primer is SYC1078 (SEQ ID NO:3).

35. (New) The method of Claim 21, wherein the amplification reaction is a polymerase chain reaction.

36. (New) The method of Claim 21, wherein step (3) is carried out using a probe that is complementary or substantially complementary to said amplification products.

37. (New) The method of Claim 36, wherein said probe is selected from the group consisting of CS12 (SEQ ID NO:6), CS1 (SEQ ID NO:7) and CS3 (SEQ ID NO:8).

38. (New) A kit for identifying cancerous cells in a human sample, comprising a pair of primers, wherein said pair of primers consists of a first primer capable of hybridizing within exon 8 or downstream of exon 8 of the hTERT gene and a second primer capable of hybridizing upstream of exon 8 of the hTERT gene and instructions for identifying cancerous cells.

39. (New) The kit of Claim 38, wherein said second primer is capable of hybridizing within exon 7 of the hTERT gene.

40. (New) The kit of Claim 38, wherein said second primer is capable of hybridizing within exon 6 of the hTERT gene.

41. (New) The kit of Claim 38, wherein said second primers are SYC1118 (SEQ ID NO:5) or SYC1076 (SEQ ID NO:2).

42. (New) The kit of Claim 38, wherein said first primers are SYC1097 (SEQ ID NO:4) or SYC1078 (SEQ ID NO:3).

43. (New) The kit of Claim 38, further comprising a probe capable of hybridizing at a sequence encompassing the exon 7- exon 8 splice junction.

44. (New) The kit of Claim 38, further comprising a probe selected from the group consisting of CS12 (SEQ ID NO:6), CS1 (SEQ ID NO:7), or CS3 (SEQ ID NO:8) and instructions for identifying cancerous cells.

45. (New) The kit of Claim 38, comprising a pair of primers SYC1118 (SEQ ID NO:5) and SYC1097 (SEQ ID NO:4), a probe that is CS12 (SEQ ID NO:6) and instructions for identifying cancerous cells.